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     (FILE 'HOME' ENTERED AT 15:03:14 ON 06 SEP 2001)

     FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, GENBANK' ENTERED AT 15:03:41 ON
06
     SEP 2001
L1       155524 S GENE?(P)REPLAC?
L2          538 S L1 (P)MRNA (P)CAP?
L3          212 S L2 (P)5
L4           24 S L3 (P)TRANSFORM?
L5            7 DUPLICATE REMOVE L4 (17 DUPLICATES REMOVED)
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L7 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2001 ACS
AN 2000:589929 CAPLUS
DN 133:172151
TI Screening for inhibitors of mRNA cap formation for use as antimycotics using host cells with fungal or mammalian capping enzymology
IN Shuman, Stewart
PA USA
SO U.S., 62 pp.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 3

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 6107040	A	20000822	US 1998-188579	19981109
	US 6232070	B1	20010515	US 1999-315444	19990520
	WO 2000063433	A1	20001026	WO 1999-US26520	19991109
	W: AU, CA, JP, MX				
	RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	EP 1127164	A1	20010829	EP 1999-962733	19991109
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
PRAI	US 1998-188579	A2	19981109		
	US 1999-315444	A	19990520		
	WO 1999-US26520	W	19991109		

AB This invention provides methods for the discovery of mols. that target an essential aspect of eukaryotic **gene** expression-the formation of the **mRNA 5' cap** m7GpppN. An underlying principle of this invention is the use of a different strains of a test organism that differ only in the compn. or source of the essential **cap**-forming enzymes. The invention provides isogenic yeast strains that derive all their **capping** activities from **fungal** sources vs. mammalian sources. These strains form the basis of a differential growth inhibition assay to identify mols. that specifically target the **fungal capping** app. This invention also provides a method to screen in vitro for mols. that inhibit **fungal** RNA triphosphatase, an essential enzyme that catalyzes the first of three steps in **cap** synthesis. The ability of human **capping** activities to **replace** those of Saccharomyces cerevisiae is demonstrated.

RE.CNT 2
RE
(1) Ho; Molecular and Cellular Biology 1998, V18(9), P5189 CAPLUS
(2) Yue; Mammalian capping enzyme complements mutant Saccharomyces cerevisiae lacking mRNA guanylytransferase and selectively binds the elongating form of RNA polymerase 2 1997, V94, P12898 CAPLUS

L7 ANSWER 4 OF 4 MEDLINE DUPLICATE 2
AN 1999278431 MEDLINE
DN 99278431 PubMed ID: 10347220
TI Characterization of human, Schizosaccharomyces pombe, and Candida albicans mRNA cap methyltransferases and complete replacement of the yeast capping apparatus by mammalian enzymes.
AU Saha N; Schwer B; Shuman S
CS Molecular Biology Program, Sloan-Kettering Institute, New York, New York 10021, USA.

NC GM52470 (NIGMS)
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1999 Jun 4) 274 (23) 16553-62.
Journal code: HIV; 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199907
ED Entered STN: 19990714
Last Updated on STN: 19990714
Entered Medline: 19990701
AB Human and fission yeast cDNAs encoding **mRNA** (guanine-N7) methyltransferase were identified based on similarity of the human (Hcm1p; 476 amino acids) and Schizosaccharomyces pombe (Pcm1p; 389 amino acids) polypeptides to the **cap** methyltransferase of Saccharomyces cerevisiae (Abd1p). Expression of PCM1 or HCM1 in S. cerevisiae complemented the lethal phenotype resulting from deletion of the ABD1 **gene**, as did expression of the NH2-terminal deletion mutants PCM1(94-389) and HCM1(121-476). The CCM1 **gene** encoding Candida albicans **cap** methyltransferase (Ccm1p; 474 amino acids) was isolated from a C. albicans genomic library by selection for complementation of the conditional growth phenotype of S. cerevisiae abd1-ts mutants. Human **cap** methyltransferase was expressed in bacteria, purified, and characterized. Recombinant Hcm1p catalyzed quantitative S-adenosylmethionine-dependent conversion of GpppA-**capped** poly(A) to m7GpppA-**capped** poly(A). We identified by alanine-scanning mutagenesis eight amino acids (Asp-203, Gly-207, Asp-211, Asp-227, Arg-239, Tyr-289, Phe-291, and Phe-354) that are essential for human **cap** methyltransferase function in vivo. All eight residues are conserved in other cellular **cap** methyltransferases. Five of the mutant human proteins (D203A, R239A, Y289A, F291A, and F354A) were expressed in bacteria and found to be defective in **cap** methylation in vitro. Concordance of mutational effects on Hcm1p, Abd1p, and vaccinia **capping** enzyme underscores a conserved structural basis for **cap** methylation in DNA viruses, yeast, and metazoans. This is in contrast to the structural and mechanistic divergence of the RNA triphosphatase components of the yeast and metazoan **capping** systems. Nevertheless, we demonstrate that the entire three-component yeast **capping** apparatus, consisting of RNA **5'**-triphosphatase (Cet1p), RNA guanylyltransferase (Ceg1p), and Abd1p could be **replaced** in vivo by the two-component mammalian apparatus consisting of a bifunctional triphosphatase-guanylyltransferase Mce1p and the methyltransferase Hcm1(121-476)p. Isogenic yeast strains with **fungal** versus mammalian **capping** systems should facilitate rational screens for antifungal drugs that target **cap** formation in vivo.

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USPT	l2 same 5	36	L3
USPT	l1 same mRNA same cap$	92	L2
USPT	gene same replac$	8727	L1

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L3: Entry 7 of 36 File: USPT Jan 16, 2001

DOCUMENT-IDENTIFIER: US 6174669 B1
TITLE: Method for making full-length cDNA libraries

BSPR:
As conventional methods for synthesizing full-length cDNAs, the following methods can be mentioned; the method utilizing a Cap binding protein of yeast or Hela cells for labeling the 5' Cap site (I. Edery et al., "An Efficient Strategy To Isolate Full-length cDNAs Based on an mRNA Cap Retention Procedure (CAPture)", MCB, 15, 3363-3371, 1995); the method where phosphates of incomplete cDNAs without 5' Cap are removed by using alkaline phosphatase and then the whole cDNAs are treated with de-capping enzyme of tobacco mosaic virus so that only the full-length cDNAs have phosphates (K. Maruyama et al., "Oligo-capping: a simple method to replace the cap structure of eukaryotic mRNAs with oligoribonucleotides", Gene, 138, 171-174, 1995., S. Kato et al., "Construction of a human full-length cDNA bank", Gene, 150, 243-250, 1995) and the like.